

**In the Claims:**

*Please amend the claims as follows:*

1. (currently amended) A method comprising:
  - receiving a first data string in an electronic ~~device~~component,
  - receiving a second data string in said electronic ~~device~~component,
  - determining pairs of consecutively following data entities in said first data string in a processing unit,
  - determining the relative positions of said pairs of consecutively following data entities in said first data string in said processing unit,
  - allocating a position label to each of said data entities in the first data string in said processing unit,
  - numbering same data entities according to their relative position in accordance with the position label in said processing unit,
  - determining similar data entities with the same order in said second data string in said processing unit,
  - determining the relative positions of said determined data entities in said second data string in said processing unit,
  - determining a matching measure by determining how far the relative positions of data entities in said second data string match with the relative positions of consecutively following data entities in said first data string in said processing unit, and
  - determining a similarity measure which corresponds to the matching measure of at least one comparison result in said processing unit,
  - repeating said determination of said similarity measure with a number of received second data strings in said processing unit, andoutputting by an interface said determined similarity measures for said data strings according to the amount of similarity to said first data string,  
wherein said first data string of entities and said second data string of entities are data strings relating to one of associative text string, genome analysis, speech recognition, and musical melody.

2. (previously presented) The method according to claim 1, further comprising:
  - determining at least one error limit for at least one of said entities, and
  - considering said at least one error limit during said determination of said matching measure.
3. (previously presented) The method according to claim 1, further comprising:
  - determining a first distance between said two data entities of consecutively following data entities in said first data string,
  - determining a second distance of said two data entities determined in said second data string,
  - determining a difference between said first and second distances, and
  - considering said difference during said determination of said matching measure.
4. (previously presented) The method according to claim 1, further comprising:
  - storing said second string together with said similarity measure.
5. (previously presented) The method according to claim 1, further comprising:
  - determining a threshold for said similarity measure, and
  - outputting said second string, if said determined similarity measure at least equals said threshold.
6. (canceled)
7. (previously presented) The method according to claim 1, further comprising:
  - analyzing the first string for entities not present in the first string, and
  - suppressing in the second string all said entities not present in said first string.
8. (previously presented) The method according to claim 7, further comprising:
  - determining the number of entities that are present in the second string, but are not

present in the first string, as a second similarity measure.

9. (previously presented) The method according to claim 8, further comprising:
  - determining a section within said second string comprising at least the same number of entities that are simultaneously present in both strings.
10. (previously presented) A computer readable medium stored with code, which when executed by a computer, performs the method of claim 1.
11. (canceled)
12. (canceled)
13. (canceled)
14. (currently amended) An electronic device comprising:
  - a component configured to receive a first data string of entities and a second data string of entities, said first data string of entities and said second data string of entities being data strings relating to one of associative text string, genome analysis, speech recognition, and musical melody,
  - a processing unit configured to
    - determine pairs of consecutively following data entities in said first data string,
    - determine the relative positions of said pairs of consecutively following data entities in said first data string,
    - allocate a position label to each of said data entities in the first data string,
    - number same data entities according to their relative position in accordance with the position label;
    - determine similar data entities with the same order in said second data string,
    - determine the relative positions of said determined data entities in said second data string, and
    - determine a matching measure by determining how far the relative positions of data

- entities in said second data string match with the relative positions of consecutively following data entities in said first data string, and
- ~~repeating~~repeat said determination of said similarity measure with a number of received second data strings, and
  - an interface configured to output a similarity measure for said second data string and said number of second data strings according to the amount of similarity to said first data string.
15. (previously presented) An electronic device according to claim 14, further comprising a storage configured to store received strings and said determined similarity measures.
16. (previously presented) The method according to claim 1, wherein the electronic device is a mobile terminal device.
17. (previously presented) The method according to claim 1, wherein the first data string and the second data string are pieces of text.
18. (previously presented) The method according to claim 1, wherein the first data string and the second data string are each a sequence of musical notes.
19. (previously presented) The method according to claim 1, wherein the first data string and the second data string are sequences of deoxyribonucleic acid.
20. (previously presented) The method according to claim 1, wherein the first data string and the second data string are each phonetic sounds.